

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/554,068
Source: IFWO
Date Processed by STIC: 10/2/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/554,068

CRF Edit Date: 10/2/06
Edited by: W

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other: Sequence 28 - corrected the spelling of "position"



IFWO

RAW SEQUENCE LISTING

DATE: 10/02/2006

PATENT APPLICATION: US/10/554,068

TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

3 <110> APPLICANT: Kadler, Karl
 4 Bulleid, Neil
 5 Ashcroft, Gillian
 7 <120> TITLE OF INVENTION: Modified Peptides and Their Uses
 9 <130> FILE REFERENCE: 17695-0002
 11 <140> CURRENT APPLICATION NUMBER: US 10/554,068
 12 <141> CURRENT FILING DATE: 2005-10-21
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/00171
 15 <151> PRIOR FILING DATE: 2004-04-21
 17 <150> PRIOR APPLICATION NUMBER: GB 0309064.4
 18 <151> PRIOR FILING DATE: 2003-04-22
 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: PatentIn version 3.3
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 30 <223> OTHER INFORMATION: Oligonucleotide for PCR
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 36 <210> SEQ ID NO: 2
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 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Oligonucleotide for PCR
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 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Oligonucleotide for PCR
 56 <400> SEQUENCE: 3
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 60 <210> SEQ ID NO: 4
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 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Oligonucleotide for PCR

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Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

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125 <220> FEATURE:
126 <223> OTHER INFORMATION: DNA molecule based on procollagen type III N-propeptide.
127 Sequence prior to N100 replaced with the sequence for the G123
128 domains of the alpha3 chain of laminin-5 whilst retaining the
129 collagen III signal sequence.
131 <400> SEQUENCE: 9
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138 atggcagttg tggatggcca gctcacctgt gtctacaacc tgggggaccg tgaggctgaa 240
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RAW SEQUENCE LISTING

DATE: 10/02/2006

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TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

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236	caaggagaaa	gtggtcgacc	aggtcctcct	gggccatctg	gtccccgagg	tcagcctggt	3180
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DATE: 10/02/2006

PATENT APPLICATION: US/10/554,068

TIME: 11:30:02

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

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320 gaagggtgaat tcaaggctga aggaatatgc aaattcacct acacagttct ggaggatggt 5700
322 tgcacgaaac aactgggga atggagcaaa acagtctttg aatatcgaa acgcaaggct 5760
324 gtgagactac ctattgtaga tattgcaccc tatgacattg gtggtcctga tcaagaattt 5820
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329 <210> SEQ ID NO: 10
330 <211> LENGTH: 1950
331 <212> TYPE: PRT
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:

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RAW SEQUENCE LISTING

DATE: 10/02/2006

PATENT APPLICATION: US/10/554,068

TIME: 11:30:02

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Output Set: N:\CRF4\10022006\J554068.raw

335 <223> OTHER INFORMATION: Sequence of the modified pro-alpha chain

337 <400> SEQUENCE: 10

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344          20          25          30
347 Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr
348          35          40          45
351 Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val
352          50          55          60
355 Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu
356 65          70          75          80
359 Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val
360          85          90          95
363 Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn
364          100         105         110
367 Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr
368          115         120         125
371 Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu
372          130         135         140
375 Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro
376 145         150         155         160
379 Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp
380          165         170         175
383 Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn
384          180         185         190
387 Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser
388          195         200         205
391 Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln
392          210         215         220
395 Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val
396 225         230         235         240
399 Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser
400          245         250         255
403 Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser
404          260         265         270
407 Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg
408          275         280         285
411 Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp
412          290         295         300
415 Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp
416 305         310         315         320
419 Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg
420          325         330         335
423 Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys
424          340         345         350
427 Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys
428          355         360         365
431 Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006
TIME: 11:30:03

Input Set : N:\AMC\PTO.AMC.txt
Output Set: N:\CRF4\10022006\J554068.raw

fyi
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; Xaa Pos. 2,3,5,7,8,10,11

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/554,068

DATE: 10/02/2006

TIME: 11:30:03

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10022006\J554068.raw

L:2217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0

Raw Sequence Listing before editing (for reference only)



IFWO

RAW SEQUENCE LISTING

DATE: 09/29/2006

PATENT APPLICATION: US/10/554,068

TIME: 10:16:06

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

3 <110> APPLICANT: Kadler, Karl
 4 Bulleid, Neil
 5 Ashcroft, Gillian
 7 <120> TITLE OF INVENTION: Modified Peptides and Their Uses
 9 <130> FILE REFERENCE: 17695-0002
 11 <140> CURRENT APPLICATION NUMBER: US 10/554,068
 12 <141> CURRENT FILING DATE: 2005-10-21
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/00171
 15 <151> PRIOR FILING DATE: 2004-04-21
 17 <150> PRIOR APPLICATION NUMBER: GB 0309064.4
 18 <151> PRIOR FILING DATE: 2003-04-22
 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 20
 26 <212> TYPE: DNA
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 66 <223> OTHER INFORMATION: Oligonucleotide for PCR

see p. 8
**Does Not Comply
 Corrected Diskette Needed**

20

31

31

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/554,068

DATE: 09/29/2006

TIME: 10:16:06

Input Set : F:\17695-0002.txt

Output Set: N:\CRF4\09292006\J554068.raw

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77 <220> FEATURE:
78 <223> OTHER INFORMATION: Oligonucleotide for PCR
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122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: DNA molecule based on procollagen type III N-propeptide.
127 Sequence prior to N100 replaced with the sequence for the G123
128 domains of the alpha3 chain of laminin-5 whilst retaining the
129 collagen III signal sequence.
131 <400> SEQUENCE: 9
132 atgatgagct ttgtgcaaaa ggggagctgg ctacttctcg ctctgcttca tcccactatt 60
134 attttgga catctctgtc cttgtttctc caaaggccca actcaagaga aaatgggggt 120
136 actgagaata tgtttgtgat gtaccttgga aataaagatg cctcccggga ctacatcggc 180
138 atggcagttg tggatggcca gctcacctgt gtctacaacc tgggggaccg tgaggctgaa 240
140 ctccaagtgg accagatctt gaccaagagt gagactaagg aggcagttat ggatcgggtg 300

```

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142	aaatttcaga	gaatttatca	gtttgcaagg	cttaattaca	ccaaaggagc	cacatccagt	360
144	aaaccagaaa	caccgcgagt	ctatgacatg	gatggtagaa	atagcaatac	actccttaat	420
146	ttggatcctg	aaaatgttgt	attttatgtt	ggaggttacc	cacctgattt	taaacttccc	480
148	agtcgactaa	gtttccctcc	atacaaagg	tgtattgaat	tagatgacct	caatgaaaat	540
150	gttctgagct	tgtacaactt	caaaaaaaca	ttcaatctca	acacaactga	agtggagcct	600
152	tgtagaagga	ggaaggaaga	gtcagacaaa	aattattttg	aaggtagcgg	ctatgctcga	660
154	gttccaactc	aaccacatgc	tcccatccca	acctttggac	agacaattca	gaccaccgtg	720
156	gatagaggct	tgtctgttct	tgcagaaaac	ggggatcgct	tcatatctct	aaatatagaa	780
158	gatggcaagc	tcatggtgag	atacaaactg	aattcagagc	taccaaaga	gagaggagtt	840
160	ggagacgcca	taacaacgg	cagagaccat	tcgattcaga	tcaaaattgg	aaaactccaa	900
162	aagcgtatgt	ggataaatgt	ggacgttcaa	aacactataa	ttgatggtga	agtatttgat	960
164	ttcagcacat	attatctggg	aggaattcca	attgcaatca	gggaaagatt	taacatttct	1020
166	acgcctgctt	tccgaggtct	catgaaaaat	ttgaagaaaa	ccagtgggtg	cgtagatttg	1080
168	aatgatactg	tgggagtaac	caaaaagtgc	tcggaagact	ggaagcttgt	gcgatctgcc	1140
170	tcattctcca	gaggaggaca	attgagtttc	actgatttgg	gcttaccacc	tactgaccac	1200
172	ctccaggcct	catttggatt	tcagaccttt	caaccagtg	gcatattatt	agatcatcag	1260
174	acatggacaa	ggaacctgca	ggtcactctg	gaagatggtt	acattgaatt	gagcaccagc	1320
176	gatagcggcg	gcccattttt	taaattccca	cagacgtata	tggatggttt	actgcattat	1380
178	gtatctgtaa	taagcgacaa	ctctggacta	cggcttctca	tcgatgacca	gcttctgaga	1440
180	aatagcaaaa	ggctaaaaca	catttcaagt	tcccggcagt	ctctgcgtct	gggcgggagc	1500
182	aatttttgagg	gttgtattag	caatgttttt	gtccagagg	tatcactgag	tcctgaagtc	1560
184	ctagatttga	ccagtaactc	tctcaagaga	gatgtgtccc	tgggaggctg	cagtttaaac	1620
186	aaaccacctt	ttctaattgt	gcttaaagg	tctaccaggt	ttaacaagac	caagactttt	1680
188	cgtatcaacc	agctgttgca	ggacacacca	gtggcctccc	caaggagcgt	gaagggtgtg	1740
190	caagatgcta	atggtcaagg	acctcaaggc	cccaaggag	atccaggccc	tcctggtatt	1800
192	cctgggagaa	atggtgaccc	tggatttcca	ggacaaccag	gggtcccctg	ttctcctggc	1860
194	ccccctggaa	tctgtgaatc	atgcctact	ggctcctcaga	actattctcc	ccagtatgat	1920
196	tcatatgatg	tcaagtctgg	agtagcagta	ggaggactcg	caggctatcc	tggaccagct	1980
198	ggccccccag	gccctcccgg	tccccctggt	acatctggtc	atcctgggtc	ccctggatct	2040
200	ccaggatacc	aaggaccccc	tgggtgaacct	gggcaagctg	gtccttcagg	ccctccagga	2100
202	cctcctggtg	ctataggtcc	atctggtcct	gctggaaaag	atggagaatc	aggtagaccc	2160
204	ggacgacctg	gagagcgagg	attgcctgga	cctccaggta	tcaaagggtc	agctgggata	2220
206	cctggattcc	ctggtatgaa	aggacacaga	ggcttcgatg	gacgaaatgg	agaaaagggt	2280
208	gaaacaggtg	ctcctggatt	aaagggtgaa	aatggtcttc	caggcgaaaa	tggagctcct	2340
210	ggacccatgg	gtccaagagg	ggctcctggt	gagcaggagc	ggccaggact	tcctggggct	2400
212	gcaggtgctc	ggggtaatga	cggtgctcga	ggcagtgatg	gtcaaccagg	ccctcctggt	2460
214	cctcctggaa	ctgccggatt	ccctggatcc	cctggtgcta	aggggtgaagt	tggacctgca	2520
216	gggtctcctg	gttcaaatgg	tgcctctgga	caaagaggag	aacctggacc	tcagggacac	2580
218	gctggtgctc	aaggctcctc	tggccctcct	gggattaatg	gtagtctctg	tggtaaaggc	2640
220	gaaatgggtc	ccgctggcat	tcctggagct	cctggactga	tgggagcccg	gggtcctcca	2700
222	ggaccagccg	gtgctaattg	tgtcctctgga	ctgcgagggt	gtgcagggtga	gcctggtaag	2760
224	aatggtgcca	aaggagagcc	cggaccacgt	ggtgaacgcg	gtgaggctgg	tattccaggt	2820
226	gttccaggag	ctaaaggcga	agatggcaag	gatggatcac	ctggagaacc	tgggtgcaaat	2880
228	gggcttccag	gagctgcagg	agaaaggggt	gcccctgggt	tccgaggacc	tgtctggacca	2940
230	aatggcatcc	caggagaaaa	gggtcctgct	ggagagcgtg	gtgctccagg	ccctgcaggg	3000
232	cccagaggag	ctgctggaga	acctggcaga	gatggcgtcc	ctggagggtc	aggaatgagg	3060
234	ggcatgcccg	gaagtccagg	aggaccagga	agtgatggga	aaccagggcc	tcccgaaggt	3120
236	caaggagaaa	gtggtcgacc	aggtcctcct	gggccatctg	gtccccgagg	tcagcctggt	3180
238	gtcatgggct	tccccggtcc	taaaggaaat	gatggtgctc	ctggttaagaa	tggagaacga	3240

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240 ggtggccctg gaggacctgg ccctcagggt cctcctggaa agaatggtga aactggacct 3300
242 caaggacccc cagggcctac tgggcctggt ggtgacaaag gagacacagg accccctggt 3360
244 ccacaaggat tacaaggctt gcctggtaca ggtggtcctc caggagaaaa tggaaaacct 3420
246 ggggaaccag gtccaaagggt tgatgccggt gcacctggag ctccaggagg caagggtgat 3480
248 gctggtgccc ctggtgaacg tggacctcct ggattggcag gggccccagg acttagagggt 3540
250 ggagctggtc cccctggtcc cgaaggagga aagggtgctg ctggtcctcc tgggccacct 3600
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254 cctggtccaa aggggtgaaa ggggtgaacca ggcggccagg gtgctgatgg tgtcccagggt 3720
256 aaagatggcc caaggggtcc tactggtcct attggtcctc ctggcccagc tggccagcct 3780
258 ggagataagg gtgaagggtg tgcccccgga cttccaggta tagctggacc tcgtggtagc 3840
260 cctggtgaga gaggtgaaac tggccctcca ggacctgctg gtttccctgg tgctcctgga 3900
262 cagaatggtg aacctggtgg taaaggagaa agagggggtc cggtgagaa aggtgaagga 3960
264 ggccctcctg gagttgcagg accccctgga ggttctggac ctgctggtcc tcctggtccc 4020
266 caagggtgca aagggtgaac tggcagtcct ggtggacctg gtgctgctgg cttccctggt 4080
268 gctcgtggtc ttccctggtcc tcctggtagt aatggttaacc caggaccccc aggtcccagc 4140
270 ggttctccag gcaaggatgg gccccagggt cctgcggtga aactggtgc tcctggcagc 4200
272 cctggagtgt ctggacccaa aggtgatgct ggccaaccag gagagaagggt atcgctggt 4260
274 gcccaggggc caccaggagc tccaggccca cttgggattg ctgggatcac tggagcacgg 4320
276 ggtccttgca gaccaccagg catgccagggt cctaggggaa gccctggccc tcagggtgtc 4380
278 aagggtgaaa gtgggaaacc aggagctaac ggtctcagtg gagaacgtgg tccccctgga 4440
280 cccaggggtc ttccctggtc ggctggtaca gctggtgaac ctggaagaga tggaaacct 4500
282 ggatcagatg gtcttccagg ccgagatgga tctcctggtg gcaagggtga tcgtggtgaa 4560
284 aatggctctc ctggtgcccc tggcgctcct ggtcatccag gccacctgg tcctgtcggt 4620
286 ccagctggaa agagtgggtg cagaggagaa agtggccctg ctggccctgc tgggtgctcc 4680
288 ggtcctgctg gttcccgagg tgctcctggt cctcaaggcc cacgtggtga caaagggtgaa 4740
290 acagggtgaa gtggagctgc tggcatcaaa ggacatcgag gattccctgg taatccagggt 4800
292 gccccagggt ctccaggccc tgctggtcag cagggtgcaa tcggcagtc aggacctgca 4860
294 ggccccagag gacctgttg acccagtgga cctcctggca aagatggaac cagtggacat 4920
296 ccagggtcca ttggaccacc agggcctcga ggtaacagag gtgaaagagg atctgagggc 4980
298 tccccaggcc acccagggca accaggccct cctggacctc ctggtgcccc tggtccttgc 5040
300 tgtggtggtg ttggagccgc tgccattgct gggattggag gtgaaaaagc tggcggtttt 5100
302 gccccgtatt atggagatga accaatggat ttcaaaatca acaccgatga gattatgact 5160
304 tcaactcaag ctgttaatgg acaaatagaa agcctcatta gtccctgatg ttctcgtaaa 5220
306 aaccccgcta gaaactgcag agacctgaaa ttctgccatc ctgaactcaa gagtggagaa 5280
308 tactgggttg accctaacca aggatgcaaa ttggatgcta tcaaggattt ctgtaatatg 5340
310 gaaactgggg aaacatgcat aagtgccaat cctttgaatg ttccacggaa acactggtgg 5400
312 acagattcta gtgctgagaa gaaacacgtt tggtttgagg agtccatgga tgggtggtttt 5460
314 cagtttagct acggcaatcc tgaacttct gaagatgtcc ttgatgtgca gctggcattc 5520
316 cttcgacttc tctccagccg agcttcccag aacatcacat atcaactgaa aaatagcatt 5580
318 gcatacatgg atcaggccag tggaaatgta aagaaggccc tgaagctgat ggggtcaaat 5640
320 gaagggtgaat tcaaggctga aggaaatagc aaattcacct acacagttct ggaggatggt 5700
322 tgcacgaaac aactggggga atggagcaaa acagtctttg aatatcgaa acgcaaggct 5760
324 gtgagactac ctattgtaga tattgcaccc tatgacattg gtggtcctga tcaagaattt 5820
326 ggtgtggacg ttggccctgt ttgcttttta taa 5853
329 <210> SEQ ID NO: 10
330 <211> LENGTH: 1950
331 <212> TYPE: PRT
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:

```

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335 <223> OTHER INFORMATION: Sequence of the modified pro-alpha chain

337 <400> SEQUENCE: 10

```

339 Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
340 1          5          10          15
343 His Pro Thr Ile Ile Leu Ala Thr Ser Leu Ser Leu Phe Leu Gln Arg
344          20          25          30
347 Pro Asn Ser Arg Glu Asn Gly Gly Thr Glu Asn Met Phe Val Met Tyr
348          35          40          45
351 Leu Gly Asn Lys Asp Ala Ser Arg Asp Tyr Ile Gly Met Ala Val Val
352          50          55          60
355 Asp Gly Gln Leu Thr Cys Val Tyr Asn Leu Gly Asp Arg Glu Ala Glu
356 65          70          75          80
359 Leu Gln Val Asp Gln Ile Leu Thr Lys Ser Glu Thr Lys Glu Ala Val
360          85          90          95
363 Met Asp Arg Val Lys Phe Gln Arg Ile Tyr Gln Phe Ala Arg Leu Asn
364          100         105         110
367 Tyr Thr Lys Gly Ala Thr Ser Ser Lys Pro Glu Thr Pro Gly Val Tyr
368          115         120         125
371 Asp Met Asp Gly Arg Asn Ser Asn Thr Leu Leu Asn Leu Asp Pro Glu
372          130         135         140
375 Asn Val Val Phe Tyr Val Gly Gly Tyr Pro Pro Asp Phe Lys Leu Pro
376 145         150         155         160
379 Ser Arg Leu Ser Phe Pro Pro Tyr Lys Gly Cys Ile Glu Leu Asp Asp
380          165         170         175
383 Leu Asn Glu Asn Val Leu Ser Leu Tyr Asn Phe Lys Lys Thr Phe Asn
384          180         185         190
387 Leu Asn Thr Thr Glu Val Glu Pro Cys Arg Arg Arg Lys Glu Glu Ser
388          195         200         205
391 Asp Lys Asn Tyr Phe Glu Gly Thr Gly Tyr Ala Arg Val Pro Thr Gln
392          210         215         220
395 Pro His Ala Pro Ile Pro Thr Phe Gly Gln Thr Ile Gln Thr Thr Val
396 225         230         235         240
399 Asp Arg Gly Leu Leu Phe Phe Ala Glu Asn Gly Asp Arg Phe Ile Ser
400          245         250         255
403 Leu Asn Ile Glu Asp Gly Lys Leu Met Val Arg Tyr Lys Leu Asn Ser
404          260         265         270
407 Glu Leu Pro Lys Glu Arg Gly Val Gly Asp Ala Ile Asn Asn Gly Arg
408          275         280         285
411 Asp His Ser Ile Gln Ile Lys Ile Gly Lys Leu Gln Lys Arg Met Trp
412          290         295         300
415 Ile Asn Val Asp Val Gln Asn Thr Ile Ile Asp Gly Glu Val Phe Asp
416 305         310         315         320
419 Phe Ser Thr Tyr Tyr Leu Gly Gly Ile Pro Ile Ala Ile Arg Glu Arg
420          325         330         335
423 Phe Asn Ile Ser Thr Pro Ala Phe Arg Gly Cys Met Lys Asn Leu Lys
424          340         345         350
427 Lys Thr Ser Gly Val Val Arg Leu Asn Asp Thr Val Gly Val Thr Lys
428          355         360         365
431 Lys Cys Ser Glu Asp Trp Lys Leu Val Arg Ser Ala Ser Phe Ser Arg

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; Xaa Pos. 2,3,5,7,8,10,11

VERIFICATION SUMMARY

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L:2217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0

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8

<210> 28
<211> 11
<212> PRT
<213> Unknown

<220>
<223> Sequence typically found in small leucine-rich proteoglycans.

<220>
<221> MISC_FEATURE *position*
<222> (2)..(3)
<223> X at position 2 or 3 may be any amino acid.

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X at position 5 may be any amino acid.

<220>
<221> MISC_FEATURE
<222> (7)..(8)
<223> X at position 7 or 8 may be any amino acid.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X at position 10 may be any amino acid.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X at position 11 is selected from L and I only.

<400> 28

Leu Xaa Xaa Leu Xaa Leu Xaa Xaa Asn Xaa Xaa
1 5 10